



Fig.1

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Sequence information: *Saccharomyces cerevisiae* MFE-2 (SWISSPROT Q02207)
Length: 900 AA, Molecular weight: 98703 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVTGAGGG	LGKVYALAYA	SRGAKVVVND	LGGTLGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIAV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGQYK	LSRAAWPYMR	SQKFGRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINW	NSIAPLARSR	MTENVLPPII	LKQLGPEKIV	PLVLYLTHES	TKVSNSIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWKETIDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVTA	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIQIT	AISKFORVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCGQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNYAMLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLDDN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAHVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPQDT	LKVKAWKQGS	VVVFQITDIT	RNVIVLDNAA	VKLSQAKSKL

Fig. 2

10060230.020102

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Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A
(G to S mutation at position 16)
Length: 900 AA, Molecular weight: 98733 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVITSAGGG	LGKVYALAYA	SRGAKVVVND	LGGLTGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIIV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGGYK	LSRAAWPYMR	SQKFGRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPII	LKQLGPEKIV	PLVLYLTHES	TKVSNSIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWKETIDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVTGA	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSDHV	VTEAPLIQIT	AISKFQRVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAAILGFS
490	500	510	520	530	540
KTIALEGAQR	GIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCGQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNYAMLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLDKN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAHVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPGDT	LKVKAWKQGS	VVVFQITDIT	RNVIVLDNAA	VKLSQAKSKL

Fig. 3

10060230.020102

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Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant B
(G to S mutation at position 329)
Length: 900 AA, Molecular weight: 98733 Da

10	20	30	40	50	60
MPGNLSFKDR	VVITGAGGG	LGKVYALAYA	SRGAKVVND	LGGTLGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIIV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGGYK	LSRAAWPYMR	SQKFGRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPIH	LKQLGPEKIV	PLVLYLTHES	TKVSNSIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWEITDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVTSA	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFSV
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIQIT	AISKFQRVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVV	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCGQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNyamLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLDKN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAHVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPGDT	LKVKAWKQGS	VVFQITIDTT	RNVIVLDNAA	VKLSQAKSKL

Fig. 4

10060230-020402

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Sequence information: *Saccharomyces cerevisiae* MFE-2 mutant A+B
(G to S mutation at position 16 and position 329)
Length: 900 AA, Molecular weight: 98763 Da

10	20	30	40	50	60
MPGNLSFKDR	VVVITSAGGG	LGKVYALAYA	SRGAKVVVND	LGGLTGGSGH	NSKAADLVVD
70	80	90	100	110	120
EIKKAGGIAV	ANYDSVNENG	EKIIETAIKE	FGRVDVLINN	AGILRDVSFA	KMTEREFASV
130	140	150	160	170	180
VDVHLTGGYK	LSRAAWPYMR	SQKFGRRIINT	ASPAGLFGNF	GQANYSAAKM	GLVGLAETLA
190	200	210	220	230	240
KEGAKYNINV	NSIAPLARSR	MTENVLPPII	LKQLGPEKIV	PLVLYLTHES	TKVSNISIFEL
250	260	270	280	290	300
AAGFFGQLRW	ERSSGQIFNP	DPKTYTPEAI	LNKWEITDY	RDKPFNKTQH	PYQLSDYNDL
310	320	330	340	350	360
ITKAKKLPPN	EQGSVKIKSL	CNKVVVVVTS	GGGLGKSHAI	WFARYGAKVV	VNDIKDPFVS
370	380	390	400	410	420
VEEINKLYGE	GTAIPDSHDV	VTEAPLIQIT	AISKFORVDI	LVNNAGILRD	KSFLKMKDEE
430	440	450	460	470	480
WFAVLKVHLF	STFSLSKAVW	PIFTKQKSGF	IINTTSTSGI	YGNFGQANYA	AAKAILGFS
490	500	510	520	530	540
KTIALEGAKR	GIIVNVIAPH	AETAMTKTIF	SEKELSNHFD	ASQVSPLVVL	LASEELQKYS
550	560	570	580	590	600
GRRVIGQLFE	VGGGWCGQTR	WQRSSGYVSI	KETIEPEEIK	ENWNHITDFS	RNTINPSSTE
610	620	630	640	650	660
ESSMATLQAV	QKAHSSKELD	DGLFKYTTKD	CILYNLGLGC	TSKELKYTYE	NDPDFQVLPT
670	680	690	700	710	720
FAVIPFMQAT	ATLAMDNLVD	NFNyamLLHG	EQYFKLCTPT	MPSNGTLKTL	AKPLQVLDDN
730	740	750	760	770	780
GKAALVVGGF	ETYDIKTKKL	IAYNEGSFFI	RGAVPPEKE	VRDGKRAKFA	VQNFEVPHGK
790	800	810	820	830	840
VPDFEAEIST	NKDQAALYRL	SGDFNPLHID	PTLAKAVKFP	TPILHGLCTL	GISAKALFEH
850	860	870	880	890	900
YGPYEELKVR	FTNVVFPQDT	LKVKAWKQGS	VVVFQTIDTT	RNVIVLDNAA	VKLSQAQSKL

Fig. 5

10060230.020102

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Sequence information: *Candida tropicalis* MFE-2 (SWISSPROT P22414)
Length: 906 AA, Molecular weight: 99469 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITGAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPKEVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLKNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTIVS	KDKVVLITGA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLRLAWPY	FVEKQPGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEEDD	PVWRFDDRVD	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLKVHSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKSGLI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 6

1006030-020102

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Sequence information: *Candida tropicalis* MFE-2 mutant A
(G to S mutation in position 15)
Length: 906 AA, Molecular weight: 99499 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITSAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAPFYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSRMT	ESILPPPMLE	KLGPEKVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTVSL	KDKVVLITGA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEDD	PVWRFDSDRV	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHNSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKGELI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRTGI	AINNAAIKLV
906					
GDKAKI					

Fig. 7

10050230-020102

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Sequence information: Candida tropicalis MFE-2 mutant B
(G to S mutation in position 329)
Length: 906 AA, Molecular weight: 99499 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITGAGGGL	GKYYSLEFAK	LGAKVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLDGDK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYKLVID
130	140	150	160	170	180
VHLNGAFAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPVKVAPL	VLYLSSAENE	LTGQFFEVA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTVSL	KDKVVLITSA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGA	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEED	PVWRFDDR	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHVS	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKSGLI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPIH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRGTI	AINNAAIKLV
906					
GDKAKI					

Fig. 8

10060230.020102

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Sequence information: *Candida tropicalis* MFE-2 mutant A+B
(G to S mutation in position 15 and position 329)
Length: 906 AA, Molecular weight: 99529 Da

10	20	30	40	50	60
MSPVDFKDKV	VIITSAGGGL	GKYYSLEFAK	LGAKVVVNDL	GGALNGQGGN	SKAADVVVDE
70	80	90	100	110	120
IVKNGGVAVA	DYNNVLGDGK	IVETAVKNFG	TVHVIINNAG	ILRDASMKKM	TEKDYLVID
130	140	150	160	170	180
VHLNGAFVAVT	KAAPYFQKQ	KYGRIVNTSS	PAGLYGNFGQ	ANYASAKSAL	LGFAETLAKE
190	200	210	220	230	240
GAKYNIKANA	IAPLARSMT	ESILPPPMLE	KLGPKEVAPL	VLYLSSAENE	LTGQFFEVAA
250	260	270	280	290	300
GFYAQIRWER	SGGVLFKPDQ	SFTAEEVAKR	FSEILDYDDS	RKPEYLNQY	PFMLNDYATL
310	320	330	340	350	360
TNEARKLPAN	DASGAPTVSL	KDKVVLITSA	GAGLGKEYAK	WFAKYGAKVV	VNDFKDATKT
370	380	390	400	410	420
VDEIKAAGGE	AWPDQHDVAK	DSEAIKNVI	DKYGTIDILV	NNAGILRDRS	FAKMSKQEW
430	440	450	460	470	480
SVQQVHLIGT	FNLSRLAWPY	FVEKQFGRII	NITSTSGIYG	NFGQANYSSS	KAGILGLSKT
490	500	510	520	530	540
MAIEGAKNNI	KVNIVAPHA	TAMTLTIFRE	QDKNLYHADQ	VAPLLVYLGT	DDVPVTGETF
550	560	570	580	590	600
EIGGGWIGNT	RWQRAKGAVS	HDEHTTVEFI	KEHLNEITDF	TTDTENPKST	TESSMAILSA
610	620	630	640	650	660
VGGDDDDDE	DEEEDGDEE	EDEEDEEDD	PVWRFDDR	ILYNIALGAT	TKQLKYVYEN
670	680	690	700	710	720
DSDFQVIPTF	GHLITFNSGK	SQNSFAKLLR	NFNPMLLLHG	EHYLVHSWP	PPTEGEIKTT
730	740	750	760	770	780
FEPIATTPKG	TNVVIVHGSK	SVDNKGELI	YSNEATYFIR	NCQADNKVYA	DRPAFATNQF
790	800	810	820	830	840
LAPKRAPDYQ	VDVPVSEDLA	ALYRLSGDRN	PLHIDPNFAK	GAKFPKPILH	GMCTYGLSAK
850	860	870	880	890	900
ALIDKFGMFN	EIKARFTGIV	FPGETLRVLA	WKESDDTIVF	QTHVVDRTGI	AINNAAIKLV
906					
GDKAKI					

Fig. 9

10050230.020102

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Sequence information: human 17-beta-hydroxysteroid dehydrogenase 4
(SWISSPROT P51659) (same protein as human MFE-2)
Length: 736 AA, Molecular weight: 79686 Da

10	20	30	40	50	60
MGSP	LRFDGR	VVLVTGAGAG	LGRAYALAF	ERGA	LVVVND
10	20	30	40	50	60
LGGDFKGVGK	GSLAADKVVE				
70	80	90	100	110	120
EIRRRGGKAV	ANYDSVEEGE	KVKKTALDAF	GRIDVVVNN	GILRDRSFAR	ISDEDWDIIH
130	140	150	160	170	180
RVHLRGSFQV	TRAAWEHMKK	QKYGRIIMTS	SASGIYGNFG	QANYSAAKLG	LLGLANSLAI
190	200	210	220	230	240
EGRKSNIHCH	TIAPNAGSRM	TQTVMPEDLV	EALKPEYVAP	LVLWLCHESC	EENGGLFEVG
250	260	270	280	290	300
AGWIGKLWE	RTLGAIVRQK	NHPMTPEAVK	ANWKKICDFE	NASKPQSIQE	STGSIIEVLS
310	320	330	340	350	360
KIDSEGGVSA	NHTSRATSTA	TSGFAGAIGQ	KLPPFSYAYT	ELEAIMYALG	VGASIKDPKD
370	380	390	400	410	420
LKFIYEGSSD	FSCLPTFGVI	IGQKSMGGG	LAEIPGLSIN	FAKVLHGEQY	LELYKPLPRA
430	440	450	460	470	480
GKLKCEAVVA	DVLDKGSGVV	IIMDVYSYSE	KELICHNQFS	LFLVGGGFG	GKRTSDKVKV
490	500	510	520	530	540
AVAIPNRPPD	AVLTDTTSLN	QAALYRLSGD	WNPLHIDPNF	ASLAGFDKPI	LHGLCTFGFS
550	560	570	580	590	600
ARRVLQQFAD	NDVSRFKAIK	ARFAKPVYPG	QTLQTEMWKE	GNRIHFQTKV	QETGDIVISN
610	620	630	640	650	660
AYVDLAPTSG	TSKTPSEGG	KLQSTFVPFEE	IGRRLKDIGP	EVVKVNAVF	EWHTKGGNI
670	680	690	700	710	720
GAKWTIDLKS	GSGKVYQGPA	KGAADTTIIL	SDEDFMEVVL	GKLDPPQKAF	SGRLKARGNI
730	736				
MLSQKLQMIL	KDYAKL				

Fig. 10

10060230.020402

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Sequence information: human 17-beta-hydroxysteroid dehydrogenase 4
mutant (G to S mutation at position 16)
Length: 736 AA, Molecular weight: 79686 Da

10	20	30	40	50	60
MGSP	LRFDGR	VVLVTSAGAG	LGRAYALAF	ER	GALVVVND
70	80	90	100	110	120
EIRRR	GGKAV	ANYDSVEEGE	KVVKTALDAF	GRIDVVV	NNA
130	140	150	160	170	180
RVHLR	GSFQV	TRAAWEHMKK	QKYGRIIMTS	SASGIYGNFG	QANYSAAKLG
190	200	210	220	230	240
EGRKS	NIHCN	TIAPNAGSRM	TQTVMPEDLV	EALKPEYVAP	LVLWLCHESC
250	260	270	280	290	300
AGWIG	KLRWE	RTLGAIVRQK	NHPMTPEAVK	ANWKKICDFE	NASKPQSIQE
310	320	330	340	350	360
KIDSE	GGVSA	NHTSRATSTA	TSGFAGAIGQ	KLPPFSYAYT	ELEAIMYALG
370	380	390	400	410	420
LKFIY	EGSSD	FSCLPTFGVI	IGQKSMGGG	LAEIPGLSIN	FAKVLHGEQY
430	440	450	460	470	480
GK	LKCEAVVA	DVLDKSGSVV	IIMDVYSYSE	KELICHNQFS	LFLVGSGGFG
490	500	510	520	530	540
AVAIP	NRPPD	AVLTDTTSLN	QAALYRLSGD	WNPLHIDPNF	ASLAGFDKPI
550	560	570	580	590	600
ARRVL	QQFAD	NDVSRFKAIK	ARFAKPVYPG	QTLQTEMWKE	GNRIHFQTKV
610	620	630	640	650	660
AYVDL	APTSG	TSAKTPSEGG	KLQSTFVFEE	IGRRLKDIGP	EVVKVNAVF
670	680	690	700	710	720
GAKWT	IDLKS	GSGKVYQGPA	KGAADTTIIL	SDEDFMEVVL	GKLDQPQAFF
730	736				
MLSQ	KLQMIL	KDYAKL			

Fig. 11

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